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(21) International Application Number: PCT/IB98/01232 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,144 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE ED- WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published Without international search report and to be republished upon receipt of that report.
(54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN PROSTATE		
(57) Abstract The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.		

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 112..192
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq SLLFFLLLEGGXT/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

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AAGACCTCGG AACGAGAGCG CCCCAGGGGAG CTCGGAGCGC GTGCACGCGT GGCACVACGGA    60
GAAGGCVAKK RCNNNNRCTT GAAGGTTCTG TCACCTTTTG CAGTGGTCCA A ATG AGA    117
                                     Met Arg
RAA AAG TGG AAA ATG GGA GGC ATG AAA TAC ATC TTT TCG TTG TTG TTC    165
Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
-25                               -20                               -15                               -10
TTT CTT TTG CTA GAA GGA GGC KAA ACA GAG CAA GTR AMN CAT TCA GAG    213
Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu
                               -5                               1                               5
ACA TAT TGC ATG TTT CAA GAC AAG AAG TAC AGA GTG GGT GAG AGA TGG    261
Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp
                               10                               15                               20
CAT CCT TAC CTG GAA CCT TAT GGG TTG GTT TAC TGC GTG AAC TGC ATC    309
His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile
                               25                               30                               35
TGC TCA GAG RAT GGG AAT GTG CTT TGC AGC CGA GTC AGA TGT            351
Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys
40                               45                               50

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(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 68..124
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq VSIMLLLVTVSDC/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

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AAAGGCTGAG CGGGAGGAAG CGAGAGGCAT CTAAGCAGGC AGTGTTTTGC CTTACCCCCA    60

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AGTGACC ATG AGA GGT GCC ACG CGA GTC TCA ATC ATG CTC CTC CTA GTA      109
      Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val
              -15                      -10

ACT GTG TCT GAC TGT GCT GTG ATC ACA GGG GCC TGT GAG CGG GAT GTC      157
Thr Val Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val
      -5                      1                      5                      10

CAG TGT GGG GCA GGC ACC TGC TGT GCC ATC AGC CTG TGG CTT CGA GGG      205
Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly
              15                      20                      25

CTG CGG ATG TGC ACC CCG CTG GGG CGG GAA GGC GAG GAG TGC CAC CCC      253
Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro
              30                      35                      40

GGC AGC CAC AAG ATC CCC TTC TTC AGG AAA CGC AAG CAC CAC ACC TGT      301
Gly Ser His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys
              45                      50                      55

CCT TGC TTG
Pro Cys Leu
60

```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

~~(vi) ORIGINAL SOURCE:~~

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 240..302
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SALLFSLCEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

ACCTTTCTGG ACGTTGCAAA CTGTGACATA TAAAAGCTGT TAGCTGCTCC TCTAGCCAGC      60
AGCATTCAAA CCTTGCAGAG CTTTGCTCTC AGAGAGTTTG TAAAAAGACA CACTCCTCTT      120
ACAAGAGTTC ATGCTACCAC ATAGCAAAGA ACCTTAAATT TTTGAAGAA CAATATATTC      180
ATTTTGGCAT TGTGCAGAGC AAAGTAAACT CGGTGGCCTC TTCTTCTCCA CCCCTCAAR      239
ATG ATA GCR ATC TCT GCC GTC AGC AGT GCA CTC CTG TTC TCC CTT CTC      287
Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu

```

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -27..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq SLLFFLLLEGGXT/EQ
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met	Arg	Xaa	Lys	Trp	Lys	Met	Gly	Gly	Met	Lys	Tyr	Ile	Phe	Ser	Leu	
		-25					-20						-15			
Leu	Phe	Phe	Leu	Leu	Leu	Glu	Gly	Gly	Xaa	Thr	Glu	Gln	Val	Xaa	His	
	-10					-5					1				5	
Ser	Glu	Thr	Tyr	Cys	Met	Phe	Gln	Asp	Lys	Lys	Tyr	Arg	Val	Gly	Glu	
				10					15					20		
Arg	Trp	His	Pro	Tyr	Leu	Glu	Pro	Tyr	Gly	Leu	Val	Tyr	Cys	Val	Asn	
			25					30					35			
Cys	Ile	Cys	Ser	Glu	Xaa	Gly	Asn	Val	Leu	Cys	Ser	Arg	Val	Arg	Cys	
		40					45						50			

~~(2) INFORMATION FOR SEQ ID NO: 345:~~

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -19..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq VSIMLLLVTVSDC/AV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val
 -15 -10 -5

Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys
 1 5 10

Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
 15 20 25

Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
 30 35 40 45

His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
 50 55 60

Leu

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2

seq SALLFSLLEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu
 -20 -15 -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro
 -5 1 5 10

Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

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